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## RAW SEQUENCE LISTING

DATE: 09/18/2001

PATENT APPLICATION: US/09/855,750

TIME: 16:03:32

Input Set : A:\032301W1181.seq.ST25.txt

Output Set: N:\CRF3\09182001\I855750.raw

3 <110> APPLICANT: Nampoothiri, Madhavan K.  
 5 <120> TITLE OF INVENTION: Nucleotide Sequences Which Code For The fadD15 Gene  
 7 <130> FILE REFERENCE: 032301 WD 1181  
 9 <140> CURRENT APPLICATION NUMBER: 09/855,750  
 C--> 10 <141> CURRENT FILING DATE: 2001-08-31  
 12 <160> NUMBER OF SEQ ID NOS: 4  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 2300  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Corynebacterium glutamicum  
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 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: (247)..(2103)  
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 29 <222> LOCATION: (95)..(100)  
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 35 <222> LOCATION: (72)..(78)  
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 39 <220> FEATURE:  
 40 <221> NAME/KEY: RBS  
 41 <222> LOCATION: (188)..(195)  
 42 <223> OTHER INFORMATION:  
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 48 aaatacatct tttggattgg gctttggggg ggcttttata caccctgatt ggtgcagata 120  
 50 taagaagtta ttgacacact gaatacatag agaaaaattc catgtgggta aagatatgcc 180  
 52 taaagatctg accaaaaacg tgactaaaga cgtgacgaca caagtacagc caaattaaag 240  
 54 gaaagg ttg aat ttg acc atg act tca cct aat acc ctg cag gaa tac 288  
 55 Leu Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr  
 56 1 5 10  
 58 act gaa cct gcc aag tac acc atc gga gaa tct gaa acc tgc ctg acc 336  
 59 Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr  
 60 15 20 25 30  
 62 gcc ctt cta gat cag att aag act cga cct tac gga gtt ttg ttc agc 384  
 63 Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser  
 64 35 40 45  
 66 aag cct gcc aac tat gag tgg gtg aat gta act gcc aaa gaa ttt cag 432  
 67 Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln  
 68 50 55 60  
 70 gac gag gtt ttt gcg gtt gca aaa gga att att tca gtc ggc gta gag 480  
 71 Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu  
 72 65 70 75

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74  cag gga gac cgt gtc gcg ctg ctg tcc aat act cgc tat gag tgg gct      528
75  Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala
76      80                      85                      90
78  gtg ctt gat ttc gct atc tgg gcc gct ggc gca gtg agc gtg cct atc      576
79  Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile
80  95                      100                      105                      110
82  tac agc tcc tct tca ctg tcc caa att gag tgg atc att gag gat tcc      624
83  Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser
84      115                      120                      125
86  ggc gct gtt ttg gcc att acc gaa acc cct gat cat acc gac ttg atg      672
87  Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met
88      130                      135                      140
90  aag aac ctg gtc atc ggt gaa gac gga act cca gcg att aag ggt tca      720
91  Lys Asn Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser
92      145                      150                      155
94  cct tcc aag ctg cgc cgc att cta gag atc aac tct tcg gcg ttg gag      768
95  Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu
96      160                      165                      170
98  acc ttg aag ttt gag ggc cgc gag ctt tct gat gag ctg gtg tgg gaa      816
99  Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu
100 175                      180                      185                      190
102 cgc att cat gca acc aag gcc gct gac ctg gcg tct ttg gtg tac acc      864
103 Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr
104      195                      200                      205
106 tct ggc aca act ggt agg ccg aag ggc tgc gag ttg tcc cac tac cac      912
107 Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His
108      210                      215                      220
110 tgg ttg gct gag gtc cga gcg ctg atc acc aat gac atc gga gcg atc      960
111 Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile
112      225                      230                      235
114 gcg atg cca ggt tca agg ttg ctc acc ttc ctt cct ttg gcg cac gtt      1008
115 Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val
116      240                      245                      250
118 ctt gct cgc gca gtg cac ttg gcc ttc gct gtc acc ggt gca acc cag      1056
119 Leu Ala Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln
120 255                      260                      265                      270
122 tcc cac tgg tct gat ttc agc acc ctt act ttg gaa ctg cag cgt tcc      1104
123 Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser
124      275                      280                      285
126 cgc ccg aac ctg att ttg ggt gtt cca cgc gtg ttt gaa aag gtc cgc      1152
127 Arg Pro Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg
128      290                      295                      300
130 aac gcc gct gct gct aat gct gct gac ggt ggc gca atc aag cgc atc      1200
131 Asn Ala Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile
132      305                      310                      315
134 atg ttt gag cgt gcc gaa aag gcg gcc att gaa tac tcc atg gct ctt      1248
135 Met Phe Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu
136      320                      325                      330
138 gat act gca gaa ggc cca agc aag tcc cag gtt atg gca cat aaa gcg      1296

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139	Asp	Thr	Ala	Glu	Gly	Pro	Ser	Lys	Ser	Gln	Val	Met	Ala	His	Lys	Ala	
140	335					340					345					350	
142	ttt	gac	aag	ctg	gtg	tac	tcc	aag	atc	cgt	gca	gct	gtc	ggt	ggc	gat	1344
143	Phe	Asp	Lys	Leu	Val	Tyr	Ser	Lys	Ile	Arg	Ala	Ala	Val	Gly	Gly	Asp	
144				355						360					365		
146	gtg	cag	tac	gcc	atc	acc	ggt	ggt	tca	gcg	atg	ggg	cag	gag	ctg	ctg	1392
147	Val	Gln	Tyr	Ala	Ile	Thr	Gly	Gly	Ser	Ala	Met	Gly	Gln	Glu	Leu	Leu	
148				370						375					380		
150	cac	ttc	ttc	cgc	ggt	gtg	ggc	atg	acc	atc	tac	gaa	ggt	tat	ggt	ctg	1440
151	His	Phe	Phe	Arg	Gly	Val	Gly	Met	Thr	Ile	Tyr	Glu	Gly	Tyr	Gly	Leu	
152			385					390					395				
154	acg	gaa	tct	gcg	gct	gct	gca	gcg	gtg	gac	ttc	act	gat	caa	aag	atc	1488
155	Thr	Glu	Ser	Ala	Ala	Ala	Ala	Ala	Val	Asp	Phe	Thr	Asp	Gln	Lys	Ile	
156		400					405					410					
158	ggc	act	gtg	ggt	aag	ccg	atg	ggt	ggc	atg	acc	atc	aag	atc	aat	gaa	1536
159	Gly	Thr	Val	Gly	Lys	Pro	Met	Gly	Gly	Met	Thr	Ile	Lys	Ile	Asn	Glu	
160	415				420					425					430		
162	gat	ggc	gaa	atc	atg	cta	aaa	ggc	gag	atg	ttg	ttc	cag	gga	tat	tgg	1584
163	Asp	Gly	Glu	Ile	Met	Leu	Lys	Gly	Glu	Met	Leu	Phe	Gln	Gly	Tyr	Trp	
164				435						440					445		
166	aac	aac	cca	gaa	gcc	aca	gca	gaa	gcc	ctc	cac	gac	ggt	tgg	ttc	aac	1632
167	Asn	Asn	Pro	Glu	Ala	Thr	Ala	Glu	Ala	Leu	His	Asp	Gly	Trp	Phe	Asn	
168			450							455					460		
170	acc	ggc	gat	ctg	ggt	gag	ctg	ttg	gag	tct	gga	cac	ctg	gtg	atc	acc	1680
171	Thr	Gly	Asp	Leu	Gly	Glu	Leu	Leu	Glu	Ser	Gly	His	Leu	Val	Ile	Thr	
172			465					470					475				
174	gga	cgt	aag	aaa	gat	ctg	atc	gtg	acc	gcg	ggc	ggc	aag	aac	gtt	tcc	1728
175	Gly	Arg	Lys	Lys	Asp	Leu	Ile	Val	Thr	Ala	Gly	Lys	Lys	Asn	Val	Ser	
176		480					485					490					
178	cca	gga	ccc	atg	gaa	gac	atc	atc	cgc	gca	cac	cca	ctg	gtc	agc	cag	1776
179	Pro	Gly	Pro	Met	Glu	Asp	Ile	Ile	Arg	Ala	His	Pro	Leu	Val	Ser	Gln	
180	495				500						505				510		
182	gcc	atg	gtg	gtg	ggc	gat	ggt	aaa	cca	ttc	gtt	ggc	ctg	ctg	gtg	acc	1824
183	Ala	Met	Val	Val	Gly	Asp	Gly	Lys	Pro	Phe	Val	Gly	Leu	Leu	Val	Thr	
184				515						520					525		
186	ttg	gat	cca	gat	atg	ttg	aag	cgg	tgg	aag	ctg	aac	cac	aac	att	gcg	1872
187	Leu	Asp	Pro	Asp	Met	Leu	Lys	Arg	Trp	Lys	Leu	Asn	His	Asn	Ile	Ala	
188			530						535						540		
190	gaa	tcc	cgc	acg	gtt	tct	gag	att	gct	act	gat	cct	gca	ctg	cgt	gcg	1920
191	Glu	Ser	Arg	Thr	Val	Ser	Glu	Ile	Ala	Thr	Asp	Pro	Ala	Leu	Arg	Ala	
192			545						550						555		
194	gaa	atc	cag	gat	gca	gtc	aac	aac	gct	aat	gcc	acg	gtg	tct	cat	tca	1968
195	Glu	Ile	Gln	Asp	Ala	Val	Asn	Asn	Ala	Asn	Ala	Thr	Val	Ser	His	Ser	
196		560					565					570					
198	gag	gcg	atc	aag	cgg	ttc	tac	atc	ctt	gat	cgc	gac	ctg	acc	gag	gaa	2016
199	Glu	Ala	Ile	Lys	Arg	Phe	Tyr	Ile	Leu	Asp	Arg	Asp	Leu	Thr	Glu	Glu	
200	575					580					585				590		
202	gcc	gac	gag	ctg	acc	cca	acg	ctg	aag	gtc	aag	cgc	aac	gtt	gtt	gtt	2064
203	Ala	Asp	Glu	Leu	Thr	Pro	Thr	Leu	Lys	Val	Lys	Arg	Asn	Val	Val	Val	

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204          595          600          605
206 cgc cgt tac gca gac gcc atc gac cac atc tac aac cga tgagtaacac      2113
207 Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
208          610          615
210 agagacccaa ttgattggg atggatcgac atggaccgc accgaagtcg gcgaagcacc      2173
212 aacacgcttc gctgtggcg tgatggagga ttgcgctac attgcagcca ctggcacgga      2233
214 cgggatgaa gagttcttta ctttgggctc aaatccgggt ctgacgtttg gtgatcccgga      2293
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220 <211> LENGTH: 619
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224 <400> SEQUENCE: 2
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231          20          25          30
234 Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser Lys Pro
235          35          40          45
238 Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu
239          50          55          60
242 Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly
243 65          70          75          80
246 Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu
247          85          90          95
250 Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser
251          100          105          110
254 Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala
255          115          120          125
258 Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn
259          130          135          140
262 Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser
263 145          150          155          160
266 Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu
267          165          170          175
270 Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu Arg Ile
271          180          185          190
274 His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr Ser Gly
275          195          200          205
278 Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His Trp Leu
279          210          215          220
282 Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile Ala Met
283 225          230          235          240
286 Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val Leu Ala
287          245          250          255
290 Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln Ser His
291          260          265          270
294 Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser Arg Pro
295          275          280          285

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298 Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg Asn Ala
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306 Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu Asp Thr
307      325      330      335
310 Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala Phe Asp
311      340      345      350
314 Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp Val Gln
315      355      360      365
318 Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu His Phe
319      370      375      380
322 Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu Thr Glu
323 385      390      395      400
326 Ser Ala Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile Gly Thr
327      405      410      415
330 Val Gly Lys Pro Met Gly Gly Met Thr Ile Lys Ile Asn Glu Asp Gly
331      420      425      430
334 Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp Asn Asn
335      435      440      445
338 Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn Thr Gly
339      450      455      460
342 Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr Gly Arg
343 465      470      475      480
346 Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser Pro Gly
347      485      490      495
350 Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln Ala Met
351      500      505      510
354 Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp
355      515      520      525
358 Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser
359      530      535      540
362 Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile
363 545      550      555      560
366 Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala
367      565      570      575
370 Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp
371      580      585      590
374 Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val Arg Arg
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378 Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
379      610      615
382 <210> SEQ ID NO: 3
383 <211> LENGTH: 24
384 <212> TYPE: DNA
385 <213> ORGANISM: Corynebacterium glutamicum
387 <400> SEQUENCE: 3
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391 <210> SEQ ID NO: 4

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VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date